SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rge.

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This page gives you Search Results detail for the Application 10751113 and Search Result us-10-751-113-3.rge.

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GenCore version 5.1.9
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```

OM nucleic - nucleic search, using sw model

List

July 25, 2006, 13:42:05; Search time 1996 Seconds (without alignments)

1601.889 Million cell updates/sec

Title:

US-10-751-113-3

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:

12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

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15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ACCESSION
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REFERENCE
  AUTHORS
            Liew, C.C., Marshall, W.E. and Zhang, H.
  TITLE
            Compositions and methods relating to osteoarthritis
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            Patent: WO 02070737-A 57884 12-SEP-2002;
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REFERENCE
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ACCESSION
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VERSION
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REFERENCE
           1 (bases 1 to 4495)
           Li, H., Gomes, P.J. and Chen, J.D.
           RAC3, a steroid/nuclear receptor-associated coactivator that is
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            Proc. Natl. Acad. Sci. U.S.A. 94 (16), 8479-8484 (1997)
  JOURNAL
           9238002
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           Chen, J.D., Li, H. and Gomes, P.J.
  TITLE
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  JOURNAL
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REFERENCE
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 AUTHORS
           Takeshita, A., Cardona, G.R., Koibuchi, N., Suen, C.S. and Chin, W.W.
            TRAM-1, A novel 160-kDa thyroid hormone receptor activator
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  JOURNAL
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LOCUS

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            Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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  TITLE
            Generation and initial analysis of more than 15,000 full-length
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  JOURNAL
            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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  CONSRTM
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  JOURNAL
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COMMENT
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site:
                            http://www-shgc.stanford.edu
            Contact:
                     (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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RESULT 7 CS032155

DEFINITION

ACCESSION

VERSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE

FEATURES

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RESULT 8 CS032413

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LOCUS

JOURNAL

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Query Match

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Query Match

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REFERENCE
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           Tomme, P.H. and van Rompaey, L.
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           Andrews, P.A., Walsh, J.A. and Gokhale, P.A.
  TITLE
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            Privalsky, M.L., Nakatani, Y. and Evans, R.M.
  TITLE
            Nuclear receptor coactivator ACTR is a novel histone
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  JOURNAL
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            Chen, H. and Evans, R.M.
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SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rni.

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  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
  CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE: 2000-04-14
  PRIOR APPLICATION NUMBER: 60/241,755
  PRIOR FILING DATE: 2000-10-20
  PRIOR APPLICATION NUMBER: 60/237,768
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/231,498
  PRIOR FILING DATE: 2000-09-08
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  TITLE OF INVENTION: AIB1, A novel steriod receptor co-activator
  FILE REFERENCE: 49944
  CURRENT APPLICATION NUMBER: US/09/125,635
  CURRENT FILING DATE: 1998-08-21
  PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
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; CURRENT FILING DATE: 2000-04-14
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; GENERAL INFORMATION:
; APPLICANT: Rosenfeld, Michael G.
; APPLICANT: Glass, Christopher K.
; APPLICANT: Rose, David W.
; APPLICANT: Torchia, Joseph
  TITLE OF INVENTION: A Transcription Factor Coactivator Protein, p/CIP
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   LOCATION: (110)..(4318)
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   AUTHORS: Joseph Torchia, David W. Rose, Juan Inostroza, Yasutomi Kamei,
   AUTHORS: Stefan Westin
   TITLE: The transcriptional co-activator p/CIP binds CBP and mediates
   TITLE: nuclear receptor function
   JOURNAL: Nature
   VOLUME: 387
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  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
  FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
  CURRENT FILING DATE: 2000-04-14
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; Publication No. US20040259114A1
; GENERAL INFORMATION:
; APPLICANT: RIEGEL, ANNA T.
  APPLICANT: REITER, RONALD
; APPLICANT: WELLSTEIN, ANTON
  TITLE OF INVENTION: COACTIVATORS IN THE DIAGNOSIS AND TREATMENT OF BREAST
  TITLE OF INVENTION: CANCER
  FILE REFERENCE: 54458-20001.00
  CURRENT APPLICATION NUMBER: US/10/751,113
  CURRENT FILING DATE: 2004-01-05
  PRIOR APPLICATION NUMBER: PCT/US02/21066
  PRIOR FILING DATE: 2002-07-03
  PRIOR APPLICATION NUMBER: 60/302,648
  PRIOR FILING DATE: 2001-07-05
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; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
  FILE REFERENCE: 4231/2005
  CURRENT APPLICATION NUMBER: US/10/242,535A
  CURRENT FILING DATE: 2002-09-12
  PRIOR APPLICATION NUMBER: US 10/085,783
  PRIOR FILING DATE: 2002-02-28
  PRIOR APPLICATION NUMBER: US 60/305,340
  PRIOR FILING DATE: 2001-07-13
  PRIOR APPLICATION NUMBER: US 60/275,017
  PRIOR FILING DATE: 2001-03-12
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; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
  APPLICANT: Liew, C.C.
  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
  FILE REFERENCE: 4231/2002
  CURRENT APPLICATION NUMBER: US/10/085,783A
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  TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; TITLE OF INVENTION: profile
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  CURRENT APPLICATION NUMBER: US/10/414,692
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; Publication No. US20030225528A1
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; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
  APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
  APPLICANT: Walker, Michael Graham
  TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
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; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
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  TITLE OF INVENTION: Pluripotential Stem Cells
  FILE REFERENCE: P101863WO
  CURRENT APPLICATION NUMBER: US/10/504,173
  CURRENT FILING DATE: 2004-08-11
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; Publication No. US20040259085A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Chawnshang
  APPLICANT: Hsing, Ann
  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PREDICTING
  TITLE OF INVENTION: PROSTATE CANCER
  FILE REFERENCE: 21108.0001U1
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SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rnpbn.

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OM nucleic - nucleic search, using sw model

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	2	27.8	55.6	7935	8	US-11-266-748A-56675	Sequence 56675, A
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; Publication No. US20060134670A1
; GENERAL INFORMATION:
  APPLICANT: Piu, Fabrice
  TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
  TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
  FILE REFERENCE: ACADIA.043A
  CURRENT APPLICATION NUMBER: US/11/283,329
  CURRENT FILING DATE: 2005-11-18
  PRIOR APPLICATION NUMBER: 60/629,811
  PRIOR FILING DATE: 2004-11-19
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    OTHER INFORMATION: SRC-3 variant 2
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; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
  APPLICANT: Mulligan, Karl
  TITLE OF INVENTION: Transcriptome Microarray Technology and
  TITLE OF INVENTION: Methods of Using the Same
  FILE REFERENCE: 55815-0102 (319189)
  CURRENT APPLICATION NUMBER: US/11/266,748A
  CURRENT FILING DATE: 2005-11-03
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  PRIOR FILING DATE: 2004-11-03
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  PRIOR FILING DATE: 2004-11-03
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  PRIOR FILING DATE: 2004-11-03
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; Publication No. US20060134670A1
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  APPLICANT: Piu, Fabrice
  TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
  TITLE OF INVENTION: HORMONE NUCLEAR RECEPTORS
  FILE REFERENCE: ACADIA.043A
  CURRENT APPLICATION NUMBER: US/11/283,329
  CURRENT FILING DATE: 2005-11-18
  PRIOR APPLICATION NUMBER: 60/629,811
  PRIOR FILING DATE: 2004-11-19
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; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
  TITLE OF INVENTION: Transcriptome Microarray Technology and
  TITLE OF INVENTION: Methods of Using the Same
  FILE REFERENCE: 55815-0102 (319189)
  CURRENT APPLICATION NUMBER: US/11/266,748A
  CURRENT FILING DATE: 2005-11-03
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  PRIOR FILING DATE: 2004-11-03
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  PRIOR FILING DATE: 2004-11-03
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  PRIOR FILING DATE: 2004-11-03
  PRIOR APPLICATION NUMBER: EP 04105507.0
  PRIOR FILING DATE: 2004-11-03
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   PRIOR FILING DATE: 2004-11-03
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  PRIOR FILING DATE: 2004-11-03
  PRIOR APPLICATION NUMBER: US 60/662,276
  PRIOR FILING DATE: 2005-03-14
  PRIOR APPLICATION NUMBER: US 60/700,293
   PRIOR FILING DATE: 2005-07-18
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
  TITLE OF INVENTION: Methods of Using the Same
  FILE REFERENCE: 55815-0102 (319189)
  CURRENT APPLICATION NUMBER: US/11/266,748A
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  PRIOR FILING DATE: 2004-11-03
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; Publication No. US20060134663A1
: GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
  TITLE OF INVENTION: Transcriptome Microarray Technology and
  TITLE OF INVENTION: Methods of Using the Same
  FILE REFERENCE: 55815-0102 (319189)
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
  TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
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SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rst.

Score HomeRetrieve ApplicationSCORE SystemSCOREComments /PageListOverviewFAQSuggestions

This page gives you Search Results detail for the Application 10751113 and Search Result us-10-751-113-3.rst.

<u>start</u>

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OM nucleic - nucleic search, using sw model

Run on: July 25, 2006, 14:15:46; Search time 2562 Seconds (without alignments)

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Title: US-10-751-113-3

Perfect score: 50

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Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

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Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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           CT346760.1 GI:79916147
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REFERENCE
            1 (bases 1 to 499)
           Humphray, S.J., Plumb, R.W. and Durham, J.L.
 AUTHORS
 TITLE
            Direct Submission
            Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
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REFERENCE
            1 (bases 1 to 230)
 AUTHORS
            Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
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  JOURNAL
            Unpublished (2003)
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            Contact: MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
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            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Heinrich-
            Heine-University, Duesseldorf/Germany) within the cDNA sequencing
            consortium of the German Genome Project. No sl sequence available.
            This clone (DKFZp781P1622) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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REFERENCE
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            Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 AUTHORS
            Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
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            Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 TITLE
            Diversification of Transcriptional Modulation: Large-scale
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  JOURNAL
            Genome Res. 16 (1), 55-65 (2006)
   PUBMED
            16344560
COMMENT
            Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
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  AUTHORS
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            Diversification of Transcriptional Modulation: Large-scale
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            Identification and Characterization of Putative Alternative
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            Genome Res. 16 (1), 55-65 (2006)
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COMMENT
            Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
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Fax: 81-438-52-3986
           Email: flj-cdna@nifty.com
           NEDO human cDNA project (New Energy and Industrial Technology
           Developmental Organization, Japan); cDNA library construction:
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                                               mRNA
                                                       linear
           TCAAP1E7316 Pediatric acute myelogenous leukemia cell (FAB M1)
           Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP7316, mRNA
            sequence.
ACCESSION
           BM146766
           BM146766.1 GI:17165979
VERSION
KEYWORDS
           EST.
SOURCE
           Homo sapiens (human)
 ORGANISM
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE
              (bases 1 to 537)
           Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,
 AUTHORS
           Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
            Pediatric Leukemia cDNA Sequencing Project (2001)
 JOURNAL
           Unpublished (2001)
COMMENT
           Contact: Dr. Judith F. Margolin
            Texas Children's Cancer Center and Human Genome Sequencing Center
           at Baylor College of Medicine
           1102 Bates, MC3-3320 Houston, TX 77030, USA
           Tel: 832-824-4536
           Fax: 832-825-4038
           Email: clones@txccc.org
           Seq primer: M13 primer.
FEATURES
                     Location/Qualifiers
                     1. .537
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TCAAP7316"
                     /sex="male"
                     /tissue_type="leukopheresis"
                     /cell type="myeloid cell"
                     /dev_stage="pediatric 6 years"
                     /lab host="DH10B"
                     /clone_lib="Pediatric acute myelogenous leukemia cell (FAB
                     M1) Baylor-HGSC project=TCAA"
                     /note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
                     First strand cDNA was primed with an anchored
                     XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGGCGCGCAGGAGGAG(T)VN
                     3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand
                     was primed with a BamH1-dC primer
                     [5'AGAGAGCTCGGATCCGCGGCCGCAATAATAATAAT (C) 3'].
                     Double-stranded cDNA was then digested with BamHl and XhoI
                     and directionally cloned into the BamH1 and SalI sites of
```

SCORE Search Results Details for Application 10751113 and Search Result us-10-751-113-3.rng.

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OM nucleic - nucleic search, using sw model

Run on:

July 25, 2006, 13:36:50; Search time 289 Seconds (without alignments)

1206.271 Million cell updates/sec

US-10-751-113-3

Perfect score: 50

Sequence:

1 tgccatgtgatactccagga.....actatttccaatgatgatga 50

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched:

5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:

10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 8:* 1: geneseqn1980s:* 2: geneseqn1990s:* 3: geneseqn2000s:* 4: geneseqn2001as:* 5: geneseqn2001bs:* 6: geneseqn2002as:* 7: geneseqn2002bs:* 8: geneseqn2003as:* 9: geneseqn2003bs:* 10: geneseqn2003cs:* 11: geneseqn2003ds:* 12: geneseqn2004as:*

13: geneseqn2004bs:* 14: geneseqn2005s:* 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

¥ Result Query No. Score Match Length DB ID Description 50 8 ABX11900 Abx11900 Human AIB 27.8 55.6 4239 14 ADV43475 Adv43475 Human psy

```
3
         27.8
                55.6
                        4263 12 ADJ92834
                                                             Adj92834 Human co-
                        4495 14 AEC82913
                                                             Aec82913 Breast ca
         27.8
                55.6
         27.8
                55.6
                        4789 2 AAX80992
                                                             Aax80992 Human ste
                        6754 4 AAF26490
6754 10 ADK67037
         27.8
    6
                55.6
                                                            Aaf26490 Human SRC
         27.8
                55.6
                                                             Adk67037 Gene #127
         27.8
                55.6
                        6754 14 ADY15855
                                                             Ady15855 DNA encod
    9
         27.8
                        6754 14 ADY16113
                55.6
                                                            Ady16113 DNA encod
                55.6
   10
         27.8
                        6754 14 ADY16117
                                                             Ady16117 DNA encod
         27.8
                55.6
                        6832 6 AAD30439
                                                           Aad30439 Human amp
   11
                        6835 2 AAV99915
6835 14 ADY19927
         27.8
   12
                55.6
                                                           Aav99915 AIB1 (Amp
         27.8
                55.6
                                                             Ady19927 DNA encod
                        6835 14 AED18120
                                                             Aed18120 Fibrotic
   14
         27.8
                55.6
   15
         27.8
                55.6
                        6845 10 ADE76189
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                        7088 15 AEF22148
7116 10 ADE53851
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                55.6
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         27.8
                                                             Ade53851 Human pro
                55.6
   18
         27.8
                55.6
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                       8207 10 ADF81691
8207 10 ADF81690
   19
         27.8
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                                                             Adf81691 Leukaemia
   20
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                55.6
                                                             Adf81690 Leukaemia
   21
         27.8
                55.6 12414 14 AEA47654
                                                             Aea47654 Nucleotid
   22
         27.6
                         34 8 ABX11899
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                                                            Abx11899 Human AIB
                         403 9 ACH16713
   23
         26.4
                52.8
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   24
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                      86453 14 ADY25730
                                                            Ady25730 SULF rela
         26.4
                52.8 264965 12 ADN16203
52.8 268685 6 ABS56563
   25
С
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   26
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   27
                        4621 2 AAV99919
         26.2
                52.4
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35 8 ABX11898
   28
         26.2
                52.4
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   29
          25
                50.0
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                        888 13 ADR63401
   30
         24.8
                49.6
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                       1179 4 AAK87368
3361 2 AAX80993
   31
                                                           Aak87368 Human imm
         24.4
                48.8
                                                           Aax80993 Mouse ste
Abs56565 Human SUL
   32
         24.4
                48.8
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  33
         24.4
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С
  34
         24.4
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                48.4
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                48.4 110000 14 AEB39174_07
  36
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С
                                                            Continuation (8 of
                48.4 110000 14 AEB42737_12
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                        864 8 ACA36808
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                47.6
                                                            Aca36808 Prokaryot
                                                           Abq71072 Listeria
  39
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С
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   40
         23.8
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                47.6 169659 12 ADQ59434
47.6 187851 14 ADZ13735
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Adz13735 Human can
  42
         23.8
С
  43
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                47.2 11614 14 AEA61172
                                                             Aea61172 Human HRA
  44
         23.6
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                                                             Continuation (23 o
                       2000 8 ADA72724
         23.4
                46.8
                                                            Ada72724 Rice gene
```

```
RESULT 1
ABX11900
ID
     ABX11900 standard; cDNA; 50 BP.
XX
     ABX11900;
AC
XX
DΤ
     16-MAY-2003 (first entry)
XX
DE
     Human AIB1 delta3 isofrom mRNA exon 2/exon 4 junction.
XX
KW
     Human; ss; exon 2/exon 4 junction; amplified in breast cancer;
KW
     chromosome 20q; transcription factor; antisense gene therapy; transgenic;
KW
     siRNA; small inhibitory RNA; cytostatic; intestinal cancer;
KW
     head and neck cancer; metastatic tissue cancer; neuroblastoma;
KW
     ovarian cancer; pancreatic cancer; prostate cancer; stomach cancer;
KW
     breast cancer; AIB1 delta3 isoform.
XX
os
     Homo sapiens.
XX
PN
     WO2003003904-A2.
XX
PD
     16-JAN-2003.
XX
PF
     03-JUL-2002; 2002WO-US021066.
XX
PR
     05-JUL-2001; 2001US-0302648P.
XX
     (GEOU ) UNIV GEORGETOWN MEDICAL CENT.
```

```
XX
ΡI
     Riegel AT, Reiter R, Wellstein A;
XX
DR
    WPI; 2003-221517/21.
XX
    New isolated AIB1 isoform as co-activator that potentiates
PT
PT
    transcriptional activity of nuclear hormone receptors, useful for the
PT
     diagnosis, prevention and/or treatment of cancers, in particular breast
PΫ́
    cancer.
XX
PS
    Example 6; Fig 9; 47pp; English.
XX
CC
    The invention relates to an isolated isoform of an amplified in breast
CC
    cancer 1 (AIB1) transcriptional co-activator. Also included are an
CC
    isolated nucleic sequences that encodes the isoform, a vector that
CC
    contains the nucleic acid, a recombinant cell that contains the nucleic
CC
     acid, a diagnostic kit for the detection of cancer (comprising chemical
CC
     substances that are specifically reactive to the AIB1 isoform or the
CC
    nucleic acid), an anti-AIB1 isoform antibody (or antibody fragment),
CC
    detection of cancer in a patient (comprising contacting a biological
CC
     sample obtained from the patient with at least one chemical substance
    that specifically binds to the AIB1 isoform or the nucleic acid, and
CC
CC
    detecting binding), a pharmaceutical composition (comprising an agent
CC
     that specifically binds to the AIB1 isoform, and prevents a co-activation
    of a transcription factor when administered to a patient), an siRNA
CC
CC
     (small inhibitory RNA) that inhibits expression of a transcriptional co-
CC
     activator protein, a transgenic animal comprising a recombinant gene that
    encodes the AIB1 isoform and creating the transgenic animal. The
CC
CC
    compositions comprising the AIB1 isoform or nucleic acids that bind to
CC
    the AIB1 isoform, are useful for the diagnosis, prevention and/or
CC
    treatment of disorders associated with the co-activator isoforms, such as
CC
    cancers of the intestines, head and neck, metastatic tissue,
CC
    neuroblastoma, ovaries, pancreas, prostate, stomach, and in particular
CC
    cancer of the breast. The gene for AIB1 is located on chromosome 20q. The
CC
    present sequence is the junction region of the AIB1 delta3 isoform mRNA
CC
     for exons 2 and 4 (unique to the delta3 isoform), which was targeted by
CC
     an siRNA
XX
    Sequence 50 BP; 18 A; 9 C; 11 G; 12 T; 0 U; 0 Other;
so
                          100.0%; Score 50; DB 8; Length 50;
                         100.0%; Pred. No. 3e-09;
  Best Local Similarity
  Matches
           50; Conservative
                                 0; Mismatches
                                                   0: Indels
                                                                 0; Gaps
                                                                             0:
            1 TGCCATGTGATACTCCAGGACAAGGGAAAAACTATTTCCAATGATGATGA 50
Qy
              1 TGCCATGTGATACTCCAGGACAAGGGAAAAACTATTTCCAATGATGATGA 50
Db
RESULT 2
ADV43475
    ADV43475 standard; cDNA; 4239 BP.
ID
XX
AC
    ADV43475;
XX
DT
    10-MAR-2005 (first entry)
XX
    Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1103.
DE
XX
KW
    microarray; psychoneuroendocrinimmune; chronic fatigue;
KW
    non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW
    cancer; neoplasm; infection; expressed sequence tag; ss.
XX
os
    Homo sapiens.
XX
PN
    WO2004108899-A2.
XX
PD
    16-DEC-2004.
XX
PF
     04-JUN-2004; 2004WO-US017686.
XX
     04-JUN-2003; 2003US-0475915P.
PR
XX
PA
     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PΙ
     Nicholson A. Vernon SD:
```

```
XX
DR
     WPI; 2005-031682/03.
XX
PT
     New microarray comprising probes for genes involved in
PT
     psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT
     condition associated with PNI activity, e.g., inflammatory or infectious
PT
XX
PS
     Claim 1; SEQ ID NO 1103; 254pp; English.
XX
    The invention relates to a new microarray which comprises probes for
CC
CC
     genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC
     microarray is useful in diagnosing a condition associated with PNI
CC
     activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC
     cancer and infection. The present sequence represents a
CC
     psychoneuroendocrinimmune gene expressed sequence tag. Note the
     specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC
CC
     SEQ ID NO 1829 are provided.
XX
    Sequence 4239 BP; 1280 A; 994 C; 979 G; 986 T; 0 U; 0 Other;
SO
                          55.6%; Score 27.8; DB 14; Length 4239;
  Best Local Similarity
                         82.1%; Pred. No. 2.8;
  Matches 32; Conservative
                                 0; Mismatches
                                                   7; Indels
                                                                             0:
Qу
           12 ACTCCAGGACAAGGGAAAAACTATTTCCAATGATGATGA 50
              243 AATAAAAGAGCAAGGAAAAACTATTTCCAATGATGATGA 281
Db
RESULT 3
    ADJ92834 standard; DNA; 4263 BP.
ID
XX
AC
     ADJ92834;
XX
{\bf DT}
     06-MAY-2004 (first entry)
XX
     Human co-activator p/CIP DNA.
DE
xx
     Nuclear receptor; therapy; diabetes; hyperlipidaemia; obesity;
KW
     atherosclerosis; human; co-activator; gene; ds.
KW
XX
os
     Homo sapiens.
XX
     US2003228607-A1.
PN
XX
PD
     11-DEC-2003.
XX
     14-APR-2003; 2003US-00414692.
PF
XX
PR
     15-APR-2002; 2002US-0372650P.
XX
PA
     (WAGN/) WAGNER B L.
PA
     (SCHU/) SCHULMAN I G.
XX
ΡI
     Wagner BL, Schulman IG;
XX
     WPI; 2004-167207/16.
DR
XX
PT
     Identifying compounds that bind to nuclear receptor and exhibit cell type
     specific actions, and useful for treating hyperlipidemia, obesity and
PT
PT
     diabetes.
XX
PS
     Claim 4; SEQ ID NO 35; 99pp; English.
XX
     The invention relates to screening methods for identifying compounds that
CC
CC
     bind to nuclear receptor and exhibit cell type specific actions. The
     invention relates to modulators having an improved therapeutic profile.
CC
     The method is useful for identifying compounds that bind to a nuclear
CC
CC
     receptor and exhibit cell type specific actions. It is also useful for
     identifying modulators of nuclear receptors that are useful in treating
CC
     diseases e.g., diabetes, hyperlipidaemia, obesity, atherosclerosis, etc.
CC
CC
     The present sequence is human co-activator DNA used to illustrate the
     method of the invention.
CC
XX
```

```
Sequence 4263 BP; 1286 A; 1003 C; 982 G; 992 T; 0 U; 0 Other;
                          55.6%; Score 27.8; DB 12; Length 4263;
  Best Local Similarity
                         82.1%; Pred. No. 2.8;
  Matches 32; Conservative
                                 0; Mismatches
                                                   7; Indels
                                                                 0; Gaps
          12 ACTCCAGGACAAGGGAAAAACTATTTCCAATGATGATGA 50
              Db
          243 AATAAAAGAGCAAGGAAAAACTATTTCCAATGATGATGA 281
RESULT 4
AEC82913
ID
    AEC82913 standard; cDNA; 4495 BP.
XX
AC
    AEC82913:
XX
    17-NOV-2005 (first entry)
DT
XX
DE
    Breast cancer associated cDNA SEQ ID NO 481.
XX
    cytostatic; gene therapy; gene expression; prognosis; diagnosis;
KW
KW
    microarray; breast tumor; endocrine disease; gynecology and obstetrics;
KW
    neoplasm; gene; ss.
XX
OS
    Homo sapiens.
XX
PN
    WO2005083429-A2.
XX
PD
    09-SEP-2005.
XX
    18-FEB-2005; 2005WO-US005711.
PF
XX
    20-FEB-2004; 2004US-00783271.
PR
PR
    08-DEC-2004; 2004US-0634430P.
XX
     (VERI-) VERIDEX LLC.
PA
XX
PΙ
    Wang Y;
XX
DR
    WPI; 2005-638946/65.
XX
PT
    Use of gene expression profiles of patient biological samples for
     assessing breast cancer, staging breast cancer, determining breast cancer
PT
PT
    patient protocol, or treating breast cancer.
XX
     Claim 41; SEQ ID NO 481; 76pp; English.
PS
XX
CC
     The invention describes use of gene expression profiles of patient
CC
    biological samples for assessing breast cancer, staging breast cancer,
CC
    determining breast cancer patient protocol, or treating breast cancer.
CC
     Also described are: a method of assessing breast cancer status; a method
CC
    of staging breast cancer patients; a method of determining breast cancer
CC
    patient protocol; a method of treating a breast cancer patient; a method
CC
    of cross validating a prognostic gene expression profile for breast
CC
    cancer patients; a method of independently validating a prognostic gene
CC
     expression profile for breast cancer patients; a gene profile obtained by
CC
     the method above; a method of generating a Relapse Hazard Score to enable
CC
    prognosis of breast cancer patients; a method of generating a breast
CC
     cancer prognostic patient report; a patient report generated by the
CC
    method above; a composition comprising at least one probe set selected
CC
     from SEQ ID NO. 1-111 or the psids corresponding to SEQ ID NO. 1-111; a
CC
     kit for conducting an assay to determine breast cancer prognosis in a
CC
    biological sample comprising materials for detecting isolated nucleic
CC
    acid sequences, their complements, or portions of a combination of genes
CC
     selected from those encoding mRNA: corresponding to SEQ ID NO. 1-111; or
CC
     recognized by the probe sets selected from psids corresponding to SEQ ID
CC
    NO. 1-111; articles for assessing breast cancer status comprising
CC
    materials for detecting isolated nucleic acid sequences, their
CC
     complements, or portions of a combination of genes selected from those
    encoding mRNA: corresponding to SEQ ID NO. 1-111 or recognized by the
CC
CC
    probe sets selected from psids corresponding to SEQ ID NO. 1-111; a
CC
    microarray or gene chip for performing the methods above; and a
    diagnostic/prognostic portfolio comprising isolated nucleic acid
CC
CC
     sequences, their complements, or portions of a combination of genes
     selected from those encoding mRNA: corresponding to SEQ ID NO. 1-111 or
```